

From raw data to single subject source analysis

From single subject source analysis to group  
statistics

Lau Moller Andersen & Mikkel Vinding  
Robert Oostenveld

Workshops @ MEG NORD 2018



# Group Analysis in FieldTrip of Time-Frequency Responses: A Pipeline for Reproducibility at Every Step of Processing, Going From Individual Sensor Space Representations to an Across-Group Source Space Representation

OPEN ACCESS

**Edited by:**

Srikantan S Nagarajan,  
University of California, San Francisco,  
United States

**Reviewed by:**

Jula Stephan,  
Mind Research Network (MRN),  
United States  
Stefania Della Penna,  
Università degli Studi G. d'Annunzio  
Chieti e Pescara, Italy

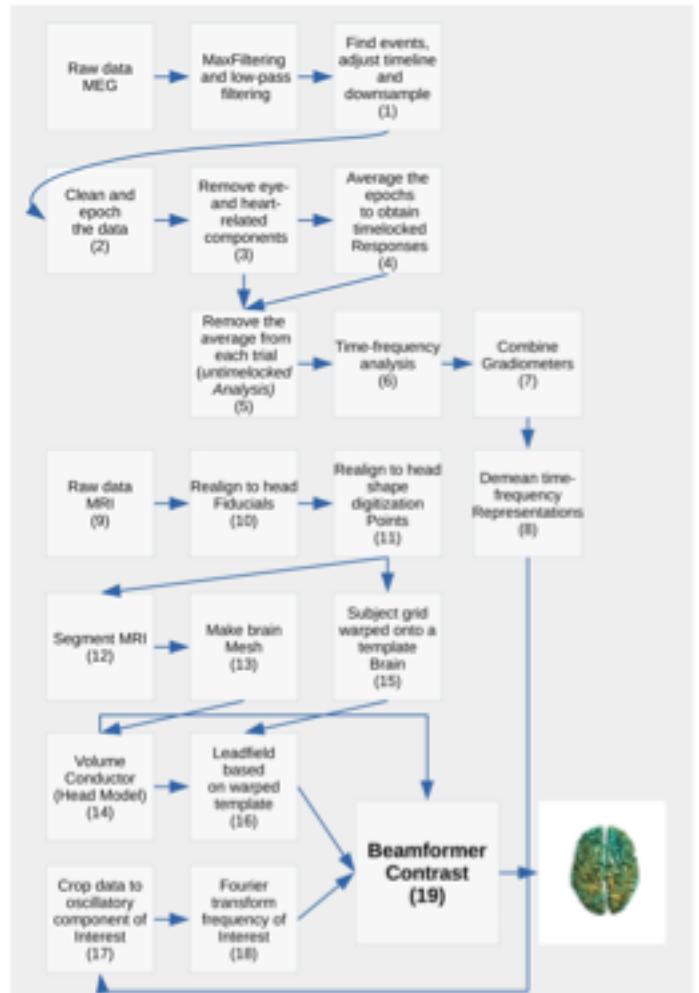
**\*Correspondence:**

Lau M. Andersen\*

NatMEG, Department of Clinical Neuroscience, Karolinska Institutet, Stockholm, Sweden

An important aim of an analysis pipeline for magnetoencephalographic (MEG) data is that it allows for the researcher spending maximal effort on making the statistical comparisons that will answer his or her questions. The example question being answered here is whether the so-called beta rebound differs between novel and repeated stimulations. Two analyses are presented: going from individual sensor space representations to, respectively, an across-group sensor space representation and an across-group source space representation. The data analyzed are neural responses to tactile stimulations

# Single Subject Pipeline

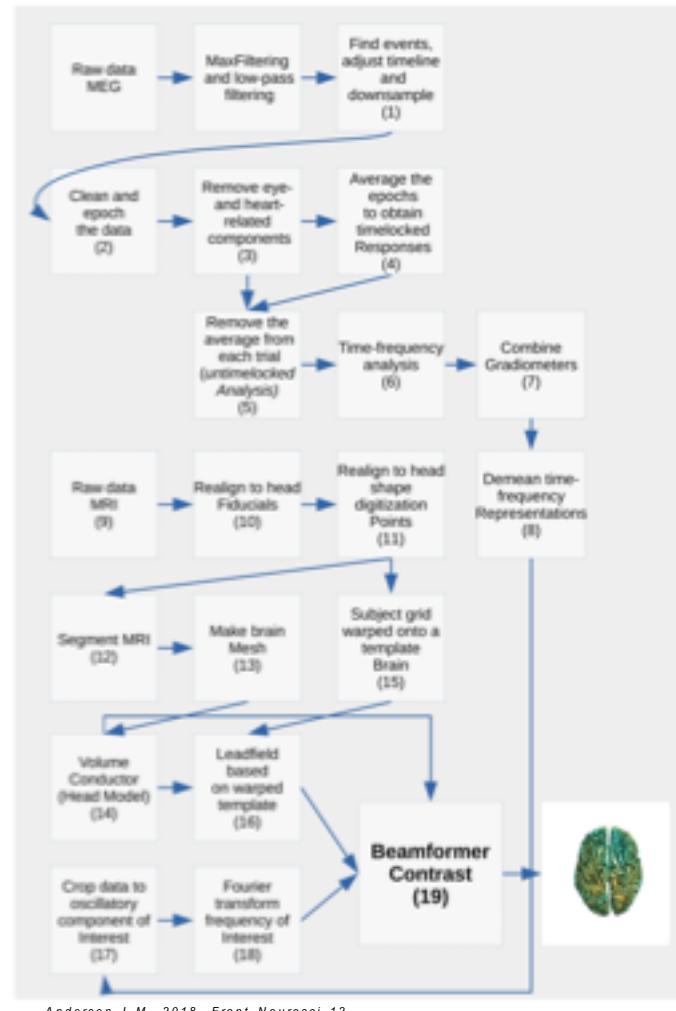


Andersen, L.M., 2018. *Front. Neurosci.* 12.

# Single Subject Pipeline

Three sections

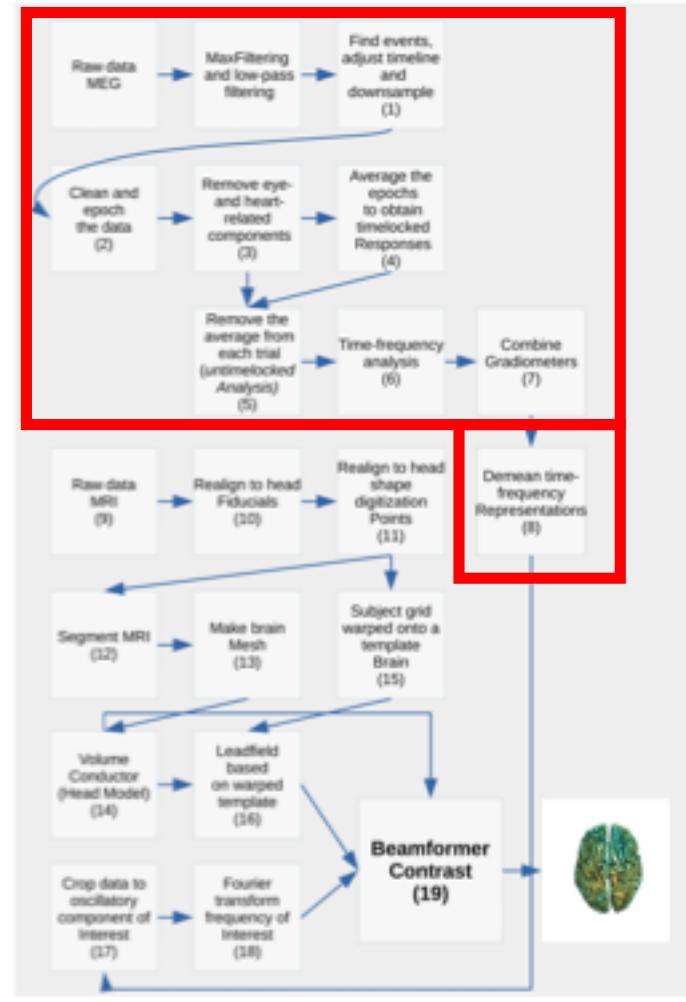
- 1) Preprocess MEG data
- 2) Preprocess MR data
- 3) Do source analysis (beamformer)



# Single Subject Pipeline

Three sections

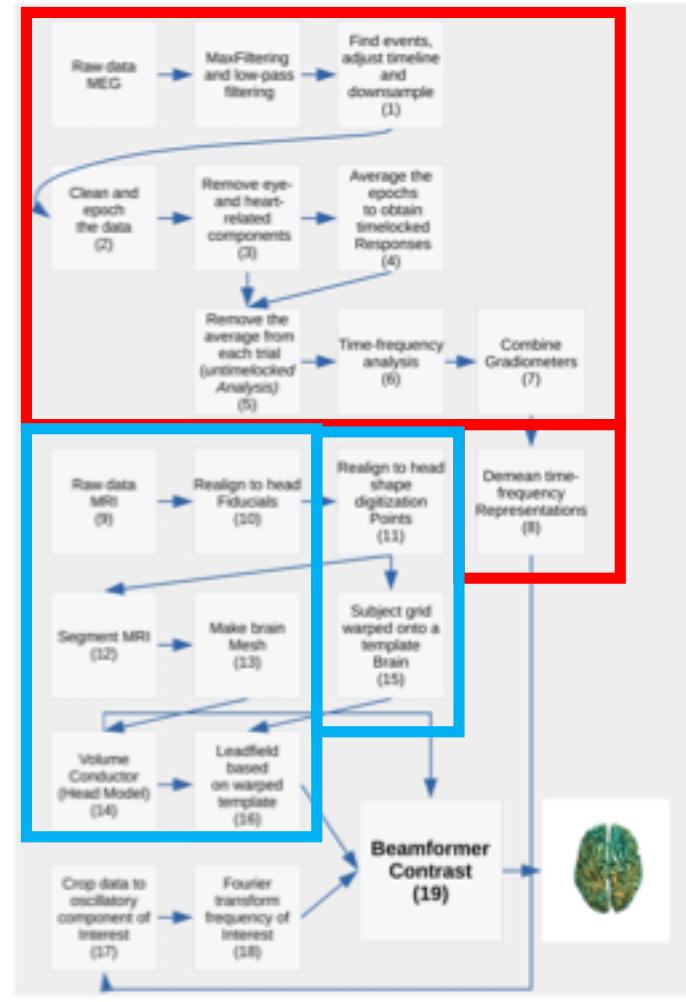
- 1) *Preprocess MEG data*
- 2) *Preprocess MR data*
- 3) *Do source analysis (beamformer)*



# Single Subject Pipeline

Three sections

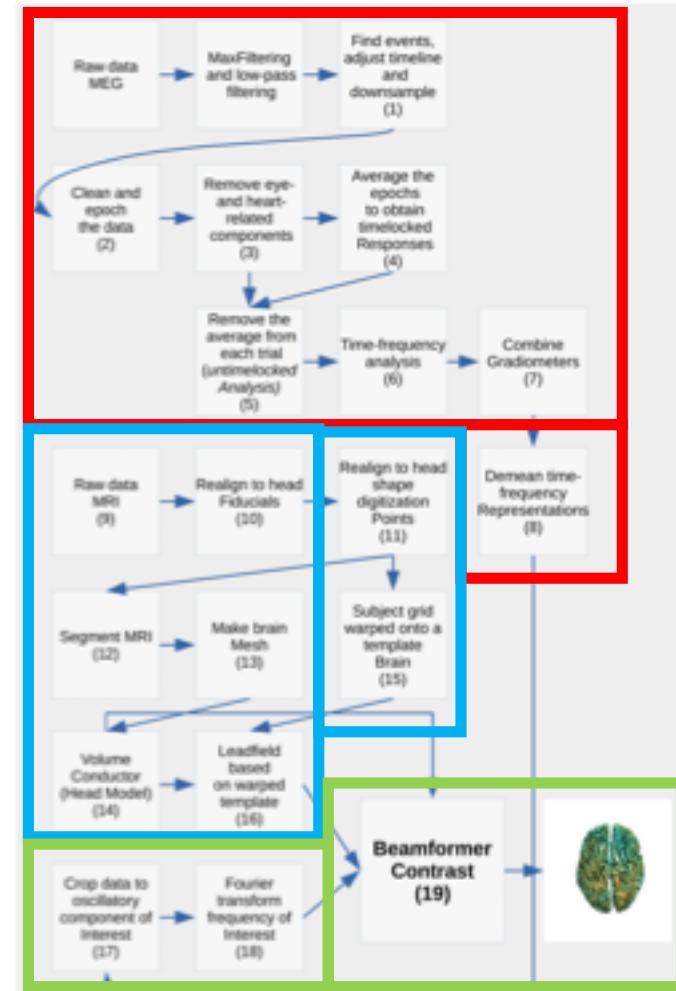
- 1) **Preprocess MEG data**
- 2) **Preprocess MR data**
- 3) **Do source analysis (beamformer)**



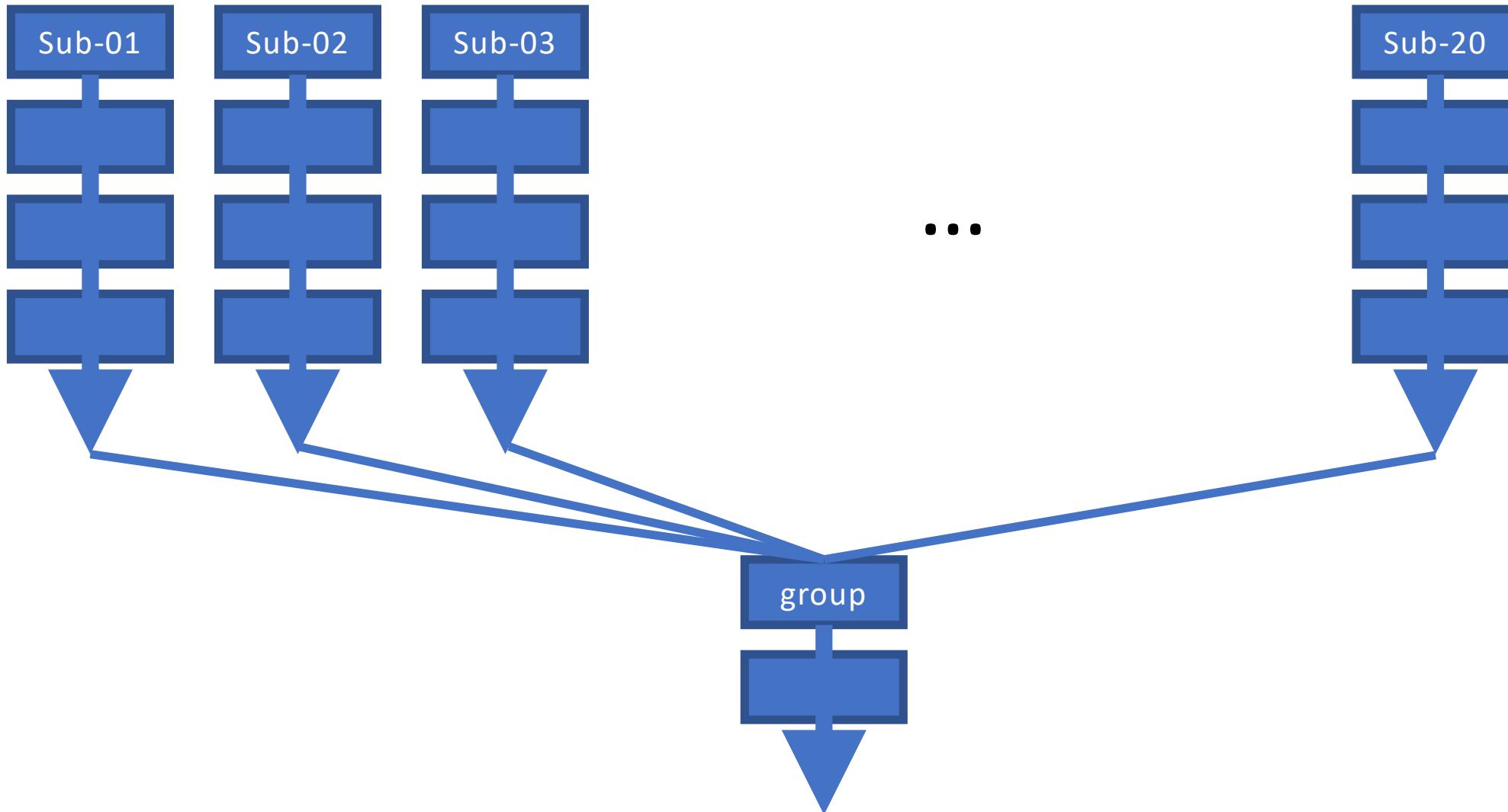
# Single Subject Pipeline

Three sections

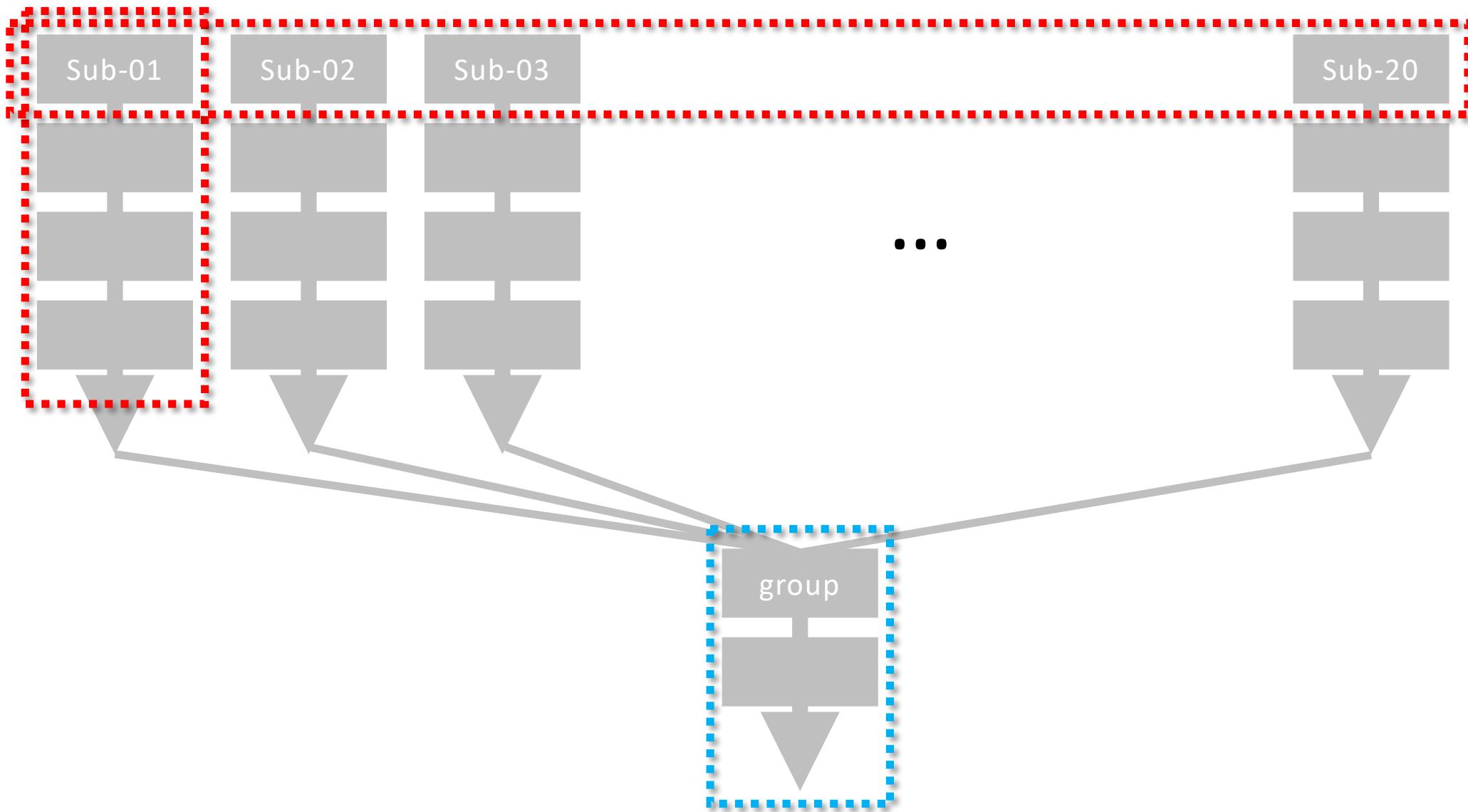
- 1) **Preprocess MEG data**
- 2) **Preprocess MR data**
- 3) **Do source analysis (beamformer)**



# Designing large scale analyses



# Running large scale analyses



# Low-level versus high-level analyses

